

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540E

DATE: 07/31/2001

TIME: 15:02:54

Input Set : A:\DX0804K.txt

Output Set: N:\CRF3\07312001\I265540E.raw

ENTERED

3 <110> APPLICANT: Parham, Christi L.  
 4 Moore, Kevin W.  
 5 Murgolo, Nicholas J.  
 6 Bazan, J. Fernando  
 8 <120> TITLE OF INVENTION: HUMAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS  
 10 <130> FILE REFERENCE: DX0804K  
 12 <140> CURRENT APPLICATION NUMBER: 09/265,540E  
 13 <141> CURRENT FILING DATE: 1999-03-08  
 15 <150> PRIOR APPLICATION NUMBER: 60/077,329  
 16 <151> PRIOR FILING DATE: 1999-03-09  
 18 <160> NUMBER OF SEQ ID NOS: 6  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1381  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (132)..(1064)  
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 35 <222> LOCATION: (567)..(567)  
 36 <223> OTHER INFORMATION: unknown nucleotide  
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 40 <221> NAME/KEY: misc\_feature  
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 42 <223> OTHER INFORMATION: unknown nucleotide  
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 54 <223> OTHER INFORMATION: unknown nucleotide  
 57 <220> FEATURE:  
 58 <221> NAME/KEY: misc\_feature  
 59 <222> LOCATION: (1369)..(1369)  
 60 <223> OTHER INFORMATION: unknown nucleotide  
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 66 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaaact 120  
 68 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170  
 69 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr  
 70 1 5 10  
 72 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218

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73	Ser	Leu	Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	
74	15					20					25						
76	gat	gaa	gtg	gcc	att	ctg	cct	gcc	cct	cag	aac	ctc	tct	gta	ctc	tca	266
77	Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	
78	30					35					40					45	
80	acc	aac	atg	aag	cat	ctc	ttg	atg	tgg	agc	cca	gtg	atc	gcg	cct	gga	314
81	Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly	
82					50					55					60		
84	gaa	aca	gtg	tac	tat	tct	gtc	gaa	tac	cag	ggg	gag	tac	gag	agc	ctg	362
85	Glu	Thr	Val	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu		
86				65					70					75			
88	tac	acg	agc	cac	atc	tgg	atc	ccc	agc	agc	tgg	tgc	tca	ctc	act	gaa	410
89	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu	
90		80						85					90				
92	ggt	cct	gag	tgt	gat	gtc	act	gat	gac	atc	acg	gcc	act	gtg	cca	tac	458
93	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr	
94		95				100						105					
96	aac	ctt	cgt	gtc	agg	gcc	aca	ttg	ggc	tca	cag	acc	tca	gcc	tgg	agc	506
97	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser	
98	110					115					120				125		
100	atc	ctg	aag	cat	ccc	ttt	aat	aga	aac	tca	acc	atc	ctt	acc	cga	cct	554
101	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	Thr	Ile	Leu	Thr	Arg	Pro	
102					130						135				140		
104	ggg	atg	gag	atc	ncc	aaa	nat	ggc	ttc	cac	ctg	gtt	att	gag	ctg	gag	602
105	Gly	Met	Glu	Ile	Xaa	Lys	Xaa	Gly	Phe	His	Leu	Val	Ile	Glu	Leu	Glu	
106				145					150					155			
108	gac	ctg	ggg	ccc	cag	ttt	gag	ttc	ctt	gtg	gcc	tac	tgg	asg	agg	gag	650
109	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	Leu	Val	Ala	Tyr	Trp	Xaa	Arg	Glu	
110			160					165					170				
112	cct	ggt	gcc	gag	gaa	cat	gtc	aaa	atg	gtg	agg	agt	ggg	ggt	att	cca	698
113	Pro	Gly	Ala	Glu	Glu	His	Val	Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	
114		175					180					185					
116	gtg	cac	cta	gaa	acc	atg	gag	cca	ggg	gct	gca	tac	tgt	gtg	aag	gcc	746
117	Val	His	Leu	Glu	Thr	Met	Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	
118	190					195					200				205		
120	cag	aca	ttc	gtg	aag	gcc	att	ggg	arg	tac	agc	gcc	ttc	agc	cag	aca	794
121	Gln	Thr	Phe	Val	Lys	Ala	Ile	Gly	Xaa	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	
122				210					215					220			
124	gaa	tgt	gtg	gar	gtg	caa	gga	gag	gcc	att	ccc	ctg	gta	ctg	gcc	ctg	842
125	Glu	Cys	Val	Glu	Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	
126				225					230					235			
128	ttt	gcc	ttt	gtt	ggc	ttc	atg	ctg	atc	ctt	gtg	gtc	gtg	cca	ctg	ttc	890
129	Phe	Ala	Phe	Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	
130			240					245						250			
132	gtc	tgg	aaa	atg	ggc	cgg	ctg	ctc	cag	tac	tcc	tgt	tgc	ccc	gtg	gtg	938
133	Val	Trp	Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	
134		255				260					265						
136	gtc	ctc	cca	gac	acc	ttg	aaa	ata	acc	aat	tca	ccc	cag	aag	tta	atc	986
137	Val	Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	

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1 38 270          275          280          285
1 40 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct      1034
1 41 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
1 42          290          295          300
1 44 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca      1084
1 45 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
1 46          305          310
1 48 ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gaggggacaa gttgtgtttc      1144
1 50 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgct tacaagtcta      1204
1 52 gaagcaacca tcagaggcag ggtggtttgt ckaacagAAC aaytgactga ggytakrggg      1264
1 54 gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga      1324
1 56 cttcatccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg      1381

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159 &lt;210&gt; SEQ ID NO: 2

160 &lt;211&gt; LENGTH: 311

161 &lt;212&gt; TYPE: PRT

162 &lt;213&gt; ORGANISM: Homo sapiens

164 &lt;220&gt; FEATURE:

165 &lt;221&gt; NAME/KEY: misc\_feature

166 &lt;222&gt; LOCATION: (146)..(146)

167 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 146 stands for Thr, Ala, Pro, or Ser.

169 &lt;220&gt; FEATURE:

170 &lt;221&gt; NAME/KEY: misc\_feature

171 &lt;222&gt; LOCATION: (148)..(148)

172 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 148 stands for Asn, Asp, His, or Tyr.

174 &lt;220&gt; FEATURE:

175 &lt;221&gt; NAME/KEY: misc\_feature

176 &lt;222&gt; LOCATION: (171)..(171)

177 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 171 stands for Arg, or Thr.

179 &lt;220&gt; FEATURE:

180 &lt;221&gt; NAME/KEY: misc\_feature

181 &lt;222&gt; LOCATION: (214)..(214)

182 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 214 stands for Arg, or Lys.

184 &lt;220&gt; FEATURE:

185 &lt;221&gt; NAME/KEY: misc\_feature

186 &lt;222&gt; LOCATION: (567)..(567)

187 &lt;223&gt; OTHER INFORMATION: unknown nucleotide

189 &lt;220&gt; FEATURE:

190 &lt;221&gt; NAME/KEY: misc\_feature

191 &lt;222&gt; LOCATION: (573)..(573)

192 &lt;223&gt; OTHER INFORMATION: unknown nucleotide

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195 &lt;221&gt; NAME/KEY: misc\_feature

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197 &lt;223&gt; OTHER INFORMATION: unknown nucleotide

199 &lt;220&gt; FEATURE:

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204 &lt;220&gt; FEATURE:

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 2 12 1 5 10 15  
 2 15 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val  
 2 16 20 25 30  
 2 19 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met  
 2 20 35 40 45  
 2 23 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
 2 24 50 55 60  
 2 27 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser  
 2 28 65 70 75 80  
 2 31 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu  
 2 32 85 90 95  
 2 35 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg  
 2 36 100 105 110  
 2 39 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
 2 40 115 120 125  
 2 43 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu  
 2 44 130 135 140  
 W-→ 2 47 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly  
 2 48 145 150 155 160  
 W-→ 2 51 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala  
 2 52 165 170 175  
 2 55 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu  
 2 56 180 185 190  
 2 59 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe  
 2 60 195 200 205  
 W-→ 2 63 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val  
 2 64 210 215 220  
 2 67 Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 2 68 225 230 235 240  
 2 71 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys  
 2 72 245 250 255  
 2 75 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro  
 2 76 260 265 270  
 2 79 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg  
 2 80 275 280 285  
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 2 84 290 295 300  
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 2 88 305 310  
 2 91 <210> SEQ ID NO: 3  
 2 92 <211> LENGTH: 1244  
 2 93 <212> TYPE: DNA  
 2 94 <213> ORGANISM: Homo sapiens  
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Input Set : A:\DX0804K.txt

Output Set: N:\CRF3\07312001\I265540E.raw

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304   Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
305     1           5           10          15
307 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc      97
308 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
309           20           25           30
311 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc     145
312 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
313           35           40           45
315 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay     193
316 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr
317           50           55           60
319 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac     241
320 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
321 65           70           75           80
323 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa     289
324 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
325           85           90           95
327 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc     337
328 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
329           100          105          110
331 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg     385
332 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
333           115          120          125
335 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg     433
336 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
337           130          135          140
339 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc     481
340 Ala Ala Leu Ala Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
341 145          150          155          160
343 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc     529
344 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
345           165          170          175
347 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac     577
348 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
349           180          185          190
351 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt     625
352 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
353           195          200          205
355 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc     673
356 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
357           210          215          220
359 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggct ctgagccgag     724
360 Gln Asn Ser Gly Ala Val Cys
361 225          230

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## VERIFICATION SUMMARY

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L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
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L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2